

Fig. 1

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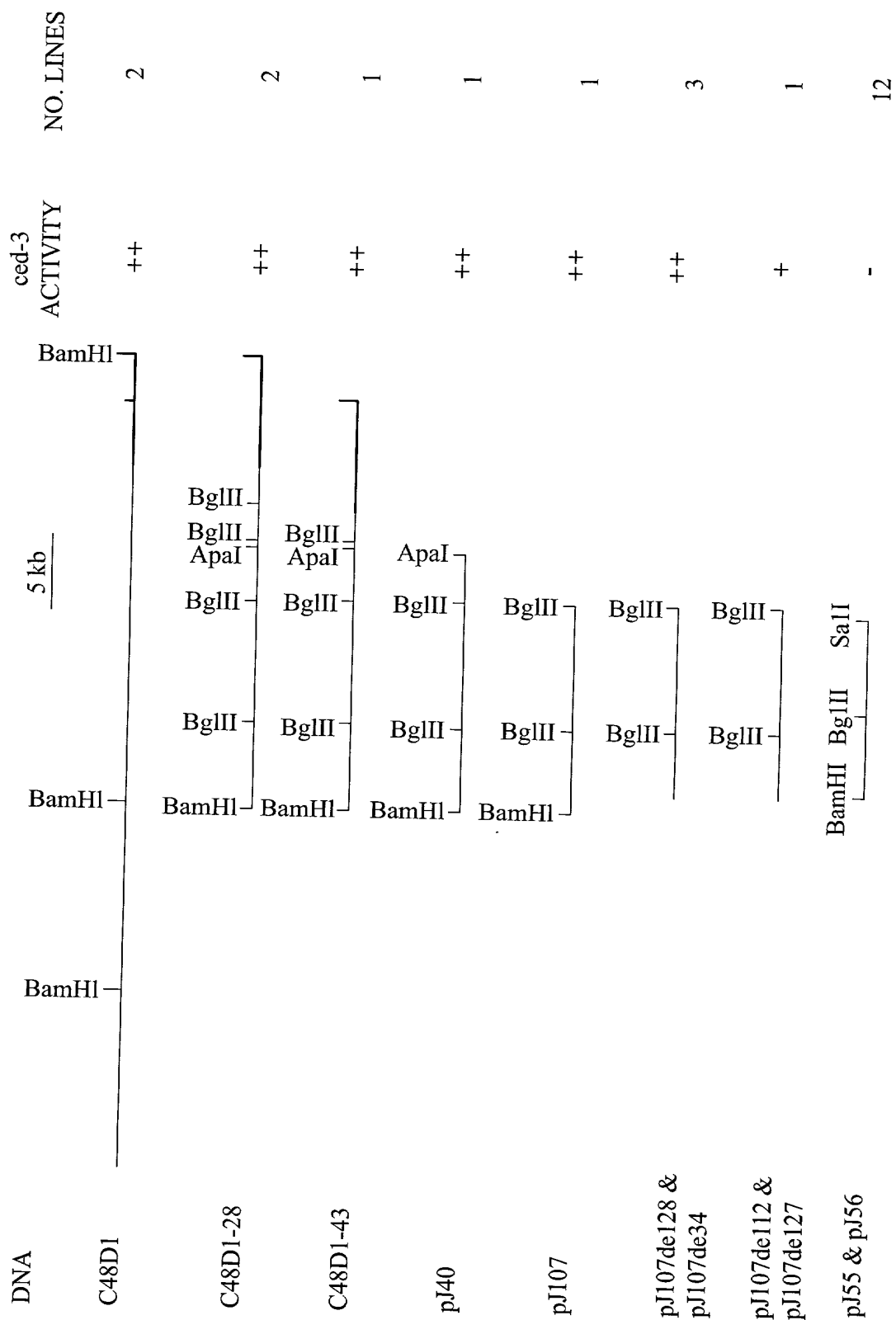


Fig. 2

*ced-3* Genomic Sequence

```

AGATCTGAAATAAGGTGATAAATTAATAAATTAAGTGTATTTCTGAGGAAATTTGACTGT
1  -----+-----+-----+-----+-----+-----+-----+ 60
TTTAGCACAATTAATCTTGTTCAGAAAAAAGTCCAGTTTTCTAGATTTTTCCGTCTTA
61  -----+-----+-----+-----+-----+-----+-----+ 120
TTGTCGAATTAATATCCCTATTATCACTTTTTCATGCTCATCCTCGAGCGGCACGTCTC
121  -----+-----+-----+-----+-----+-----+-----+ 180
AAAGAATTGTGAGAGCAAACGCGCTCCCATTTGACCTCCACACTCAGCCGCCAAAAACAAAC
181  -----+-----+-----+-----+-----+-----+-----+ 240
GTTTGAACATTCGTGTGTTGTGCTCCTTTCCGTTATCTTGCAGTCATCTTTTGTCTGTT
241  -----+-----+-----+-----+-----+-----+-----+ 300
TTTTCTTTGTTCTTTTTGTTGAACGTGTTGCTAAGCAATTATTACATCAATTGAAGAAAA
301  -----+-----+-----+-----+-----+-----+-----+ 360
GGCTCGCCGATTTATTGTTGCCAGAAAGATTCTGAGATTCTCGAAGTCGATTTTATAATA
361  -----+-----+-----+-----+-----+-----+-----+ 420
TTTAACCTTGGTTTTTGCATTGTTTCGTTTAAAAAAACCACTGTTTATGTGAAAAACGA
421  -----+-----+-----+-----+-----+-----+-----+ 480
TAGTTTACTAATAAAACTACTTTTAAACCTTTACCTTTACCTCACCGCTCCGTGTTTCATG
481  -----+-----+-----+-----+-----+-----+-----+ 540
GCTCATAGATTTTCGATACTCAAATCCAAAAATAAATTTACGAGGGCAATTAATGTGAAA
541  -----+-----+-----+-----+-----+-----+-----+ 600
CAAAAAACAATCCTAAGATTTCCACATGTTTGACCTCTCCGGCACCTTCTTCTTAGCCCC
601  -----+-----+-----+-----+-----+-----+-----+ 660
ACCACTCCATCACCTCTTTGGCGGTGTTCTTCGAAACCCACTTAGGAAAGCAGTGTGTAT
661  -----+-----+-----+-----+-----+-----+-----+ 720
CTCATTGTTGATGCTCTTTTCGATTTTATAGCTCTTTGTGCAATTTCAATGCTTTAAAC
721  -----+-----+-----+-----+-----+-----+-----+ 760
AATCCAAATCGCATTATATTTGTGCATGGAGGCAAATGACGGGGTTGGAATCTTAGATGA
781  -----+-----+-----+-----+-----+-----+-----+ 840
GATCAGGAGCTTTAGGGTAAACGCCCCGGTTCATTTTGTACCACATTTTCATCTTTCTCT
841  -----+-----+-----+-----+-----+-----+-----+ 900
GTCGTCCTTGGTATCCTCAACTTGTCCCGGTTTGTGTTTTCGGTACACTCTTCCGTGATGC
901  -----+-----+-----+-----+-----+-----+-----+ 960
CACCTGTCTCCGTCTCAATTATCGTTTAAAAATGTGAACGTGTCAGATGGGTGACTCATA
961  -----+-----+-----+-----+-----+-----+-----+ 1020
TTGCTGCTGCTACAATCCACTTTCTTTTCTCATCGGCAGTCTTACGAGCCCATCATAAAC
1021  -----+-----+-----+-----+-----+-----+-----+ 1080
TTTTTTTTTCCGCGAAATTTGCAATAAACCGGCCAAAAACTTTCTCAAATTGTTACGCAA
1081  -----+-----+-----+-----+-----+-----+-----+ 1140
TATATACAATCCATAAGAATATCTTCTCAATGTTTATGATTTCTTCGCAGCACTTTCTCT
1141  -----+-----+-----+-----+-----+-----+-----+ 1200
TCGTGTGCTAACATCTTATTTTTATAATATTCCGCTAAAATTCCGATTTTTGAGTATTA
1201  -----+-----+-----+-----+-----+-----+-----+ 1260
ATTTATCGTAAAATTATCATAATAGCACCGAAAACTACTAAAAATGGTAAAAGCTCCTTT
1261  -----+-----+-----+-----+-----+-----+-----+ 1320

```

## Repeat 1

```

=====
TAAATCGGCTCGACATTATCGTATTAAGGAATCACAAAATTCTGAGAATGCGTACTGCGC
1321 -----+-----+-----+-----+-----+-----+-----+ 1380
=====
AACATATTTGACGGCAAATATCTCGTAGCGAAAACTACAGTAATTCTTTAAATGACTAC
1381 -----+-----+-----+-----+-----+-----+-----+ 1440

```

Fig. 3

Repeat 1

```

=====>
1441 TGTAGCGCTTGTGTCGATTTACGGGCTCAATTTTTGAAAATAATTTTTTTTTTCGAATTT
-----+-----+-----+-----+-----+-----+-----+ 1500
=====
1501 TGATAACCCGTAAATCGTCACAACGCTACAGTAGTCATTTARAGGATTACTGTAGTTCTA
-----+-----+-----+-----+-----+-----+-----+ 1560
1561 GCTACGAGATATTTTGC GCGCCAAATATGACTGTAATACGCATTCTCTGAATTTTGTGTT
-----+-----+-----+-----+-----+-----+-----+ 1620
1621 TCCGTAATAATTTTCAAGATTTTGGCATTCCACTTTAAAGGCGCACAGGATTTATTCCA
-----+-----+-----+-----+-----+-----+-----+ 1680
1681 ATGGGTCTCGGCACGCAAAAAGTTTGATAGACTTTTAAATTCTCCTTGCATTTTAAATTC
-----+-----+-----+-----+-----+-----+-----+ 1740
1741 AATTACTAAAATTTTCGTGAATTTTCTGTAAATTTTAAATCAGTTTCTAATATT
-----+-----+-----+-----+-----+-----+-----+ 1800
1801 TTCCAGGCTGACAAACAGAAACAAAAACACAACAAACATTTTAAAAATCAGTTTCAAAT
-----+-----+-----+-----+-----+-----+-----+ 1860
1861 TAAAAATAACGATTTCTCATTGAAAATTGTGTTTATGTTTGCGAAAATAAAAGAGAACT
-----+-----+-----+-----+-----+-----+-----+ 1920
1921 GATTCAAACAATTTTAAACAAAAAAAACCCCAAATTCGCCAGAAATCAAGATAAAAAA
-----+-----+-----+-----+-----+-----+-----+ 1980
1981 TTCAAGAGGGTCAAATTTTCCGATTTTACTGACTTTCACCTTTTTTTTCGTAGTTCAGT
-----+-----+-----+-----+-----+-----+-----+ 2040
2041 GCAGTTGTTGGAGTTTTTGCAGAAACTAGGAAAAAATCGATAAAAAATTACTCAAATCG
-----+-----+-----+-----+-----+-----+-----+ 2100
2101 AGCTGAATTTTGAGGACAATGTTTAAAAAAAACACTATTTTCCAATAATTTCACTCAT
-----+-----+-----+-----+-----+-----+-----+ 2160

-----
TTTCAGACTAAATCGAAAATCAAATCGTACTCTGACTACGGGTCAAGTAGAGAGGTCAACC
-----
2161 -----+-----+-----+-----+-----+-----+-----+ 2220
2221 ATCAGCCGAAGATGATGCGTCAAGATAGAAGGAGCTTGCTAGAGAGGAACATTATGATGT
-----+-----+-----+-----+-----+-----+-----+ 2280
          M M R Q D R R S L L E R N I M M F
          1                                10
                    T(nl040)
2281 TCTCTAGTCATCTAAAAGTCGATGAAATTCTCGAAGTTCTCATCGCAAAACAAGTGTGA
-----+-----+-----+-----+-----+-----+-----+ 2340
          S S H L K V D E I L E V L I A K Q V L N
          20                                30
                    |intron 1
2341 ATAGTGATAATGGAGATATGATTAATGTGAGTTTTTAATCGAATAATAATTTTAAAAAAA
-----+-----+-----+-----+-----+-----+-----+ 2400
          S D N G D M I N
          40
                    |
2401 AATTGATAATATAAAGAATATTTTTGCAGTCATGTGGAACGGTTCGCGAGAAGAGACGGG
-----+-----+-----+-----+-----+-----+-----+ 2460
                    S C G T V R E K R R E
                    50

```

Fig. 3 (cont.)

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A(n718)

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AGATCGTGAAAGCAGTGCAACGACGGGAGATGTGGCGTTCGACGCGTTTTATGATGCTC
2461 -----+-----+-----+-----+-----+-----+-----+ 2520
      I  V  K  A  V  Q  R  R  G  D  V  A  F  D  A  F  Y  D  A  L
                60                                70

TTCGCTCTACGGGACACGAAGGACTTGCTGAAGTTCTTGAACCTCTCGCCAGATCGTAGG
2521 -----+-----+-----+-----+-----+-----+-----+ 2580
      R  S  T  G  H  E  G  L  A  E  V  L  E  P  L  A  R  S
                80                                90

TTTTTAAAGTTCGGCGCAAAAGCAAGGGTCTCACGAAAAAGAGGCGGATCGTAATTTT
2581 -----+-----+-----+-----+-----+-----+-----+ 2640
GCAACCCACCGGCACGGTTTTTTTCTCCGAAAATCGGAAATTATGCACCTTTCCCAAATAT
2641 -----+-----+-----+-----+-----+-----+-----+ 2700
TTGAAGTGAAATATATTTTATTTACTGAAAGCTCGAGTGATTATTTATTTTAACTA
2701 -----+-----+-----+-----+-----+-----+-----+ 2760
ATTTTCGTGGCGCAAAAGGCCATTTTGTAGATTGCGGAAAATACTTGTCACACACACAC
2761 -----+-----+-----+-----+-----+-----+-----+ 2820

ACACACATCTCCTTCAAATATCCCTTTTTCCAGTGTTGACTCGAATGCTGTCGAATTCGA
2821 -----+-----+-----+-----+-----+-----+-----+ 2880
                        V  D  S  N  A  V  E  F  E
                                100

GTGTCCAATGTCAACGGCAAGCCATCGTCGGAGCCGCGCATTGAGCCCCGCCGGCTACAC
2881 -----+-----+-----+-----+-----+-----+-----+ 2940
      C  P  M  S  P  A  S  H  R  R  S  R  A  L  S  P  A  G  Y  T
                110                                120

TTCACCGACCCGAGTTCACCGTGACAGCGTCTCTTCAGTGTCATCATTCACTTCTTATCA
2941 -----+-----+-----+-----+-----+-----+-----+ 3000
      S  P  T  R  V  H  R  D  S  V  S  S  V  S  S  F  T  S  Y  Q
                130                                140

GGATATCTACTCAAGAGCAAGATCTCGTTCTCGATCGCGTGCACTTCATTCATCGGATCG
3001 -----+-----+-----+-----+-----+-----+-----+ 3060
      D  I  Y  S  R  A  R  S  R  S  R  S  R  A  L  H  S  S  D  R
                150 1                                60

ACACAATTATTCATCTCCTCCAGTCAACGCATTTCCCAGCCAACCTTGATGTTGATGCG
3061 -----+-----+-----+-----+-----+-----+-----+ 3120
      H  N  Y  S  S  P  P  V  N  A  F  P  S  Q  P  S
                170

Repeat 1
=====
AACACTAAATTCTGAGAATGCGCACTTCAACATATTTGACGCGCAAATATCTCGTAGC
3121 -----+-----+-----+-----+-----+-----+-----+ 3180

=====
GAAAAATACAGTAACCCCTTTAAATGACTATTGTAGTGTGATTACGGGCTCGATTTTCG
3181 -----+-----+-----+-----+-----+-----+-----+ 3240

```

Fig. 3 (cont.)

```

=====
GATATGCTTATTAACACATATA
-----+-----+-----
=====
TTTTCGTTCTAGTATGCTCTAC
-----+-----+-----
=====
CATATGAATGACGAAAAATAGC
-----+-----+-----
=====
AAAAATAGTAAAAAAGCGCATGC
-----+-----+-----

```

Repeat 1  
 <=====

3301 TTGATATTTTTGATCAATTAATAAATTATTTCCGTAAACAGACACCAGCGCTACAGTACT 3360  
 -----+-----+-----+-----+-----+-----+-----+

Repeat 2

=====

3481 TTTTTCATTCAAGATATGCTTATTAACACATATAATTATCATTAAATGTGAATTTCTTG  
-----+-----+-----+-----+-----+-----+-----+ 3540

=====

TCATGTGGTTTGTTCATATGAATGACGAAAAATAGCAATTTTTTATATATTTTCCCCTAT  
3601 -----+-----+-----+-----+-----+-----+-----+ 3660

=====>  
ACGACAGCTCACTTCACATGCTGAAGACGAGAGACGCGGAGAAAATACCACACATCTTTCT  
3721 -----+-----+-----+-----+-----+-----+ 3780

=====

3841 ATGTAATAATGCATGCGTTTTTTTACACTTTCTGCACAAATGAATAGGGGGAAAATGT -----+-----+-----+-----+-----+-----+ 3900

=====

GAGCAACTTAAAAAGTAGAGAATATTAGAGCGAAAACCAAATTTCTTCAAGATATTACC  
-----+-----+-----+-----+-----+-----+ 4020

Fig. 6 (cont.)

**Fig. 3 (cont.)**

4081 -----+-----+-----+-----+-----+-----+ 4140  
 TTTTTCGATTTTCTACATCATGAATGTAGAAAATTAAAAGGGAAATCAAATTTCTA  
 4141 -----+-----+-----+-----+-----+-----+ 4200  
 GAGGATATAATTGAATGAAACATTGCGAAATTAAAATGTGCGAAACGTCAAAAAGAGGA  
 4201 -----+-----+-----+-----+-----+-----+ 4260  
  
 AATTTGGGTATCAAAATCGATCCTAAAACCAACACATTTTCAGCATCCGCCAACTCTTCAT  
 4261 -----+-----+-----+-----+-----+-----+ 4320  
 S A N S S F  
 180  
  
 TCACCGGATGCTCTTCTCTCGGATACAGTTCAAGTCGTAATCGCTCATTTCAGCAAAGCTT  
 4321 -----+-----+-----+-----+-----+-----+ 4380  
 T G C S S L G Y S S S R N R S F S K A S  
 190 200  
  
 CTGGACCAACTCAATACATATTCCATGAAGAGGATATGAACTTTGTCGATGCACCAACCA  
 4381 -----+-----+-----+-----+-----+-----+ 4440  
 G P T Q Y I F H E E D M N F V D A P T I  
 210 220  
  
 TAAGCCGTGTTTTTCGACGAGAAAACCATGTACAGAACTTCTCGAGTCCTCGTGGAATGT  
 4441 -----+-----+-----+-----+-----+-----+ 4500  
 S R V F D E K T M Y R N F S S P R G M C  
 230 240  
  
 GCCTCATCATAAATAATGAACACTTTGAGCAGATGCCAACACGGAATGGTACCAAGGCCG  
 4501 -----+-----+-----+-----+-----+-----+ 4560  
 L I I N N E H F E Q M P T R N G T K A D  
 250 260  
  
 ACAAGGACAATCTTACCAATTTGTTTCAGATGCATGGGCTATACGGTTATTTGCAAGGACA  
 4561 -----+-----+-----+-----+-----+-----+ 4620  
 K D N L T N L F R C M G Y T V I C K D N  
 270 280  
  
 | intron 4  
 ATCTGACGGGAAGGGTACGGCGAAATTATATTACCCAAACGCGAAATTTGCCATTTTGCG  
 4621 -----+-----+-----+-----+-----+-----+ 4680  
 L T G R  
  
 Repeat 3  
 =====>  
 CCGAAAATGTGGCGCCCGTCTCGACACGACAATTTGTGTAAATGCAAAAATGTATAAT  
 4681 -----+-----+-----+-----+-----+-----+ 4740  
 TTTGCAAAAACAAAATTTTGAACCTCCGCGAAAATGATTTACCTAGTTTCGAAATTTTC  
 4741 -----+-----+-----+-----+-----+-----+ 4800  
 GTTTTTTCCGGCTACATTATGTGTTTTTTCTTAGTTTTTCTATAATATTGATGTAAAAA  
 4801 -----+-----+-----+-----+-----+-----+ 4860  
 ACCGTTTGTAATTTTCAGACAATTTCCGCATACAAAACCTTGATAGCACGAAATCAATT  
 4861 -----+-----+-----+-----+-----+-----+ 4920  
 TTCTGAATTTTCAAAATTATCCAAAATGCACAATTTAAAATTTGTGAAAATTGGCAAAC  
 4921 -----+-----+-----+-----+-----+-----+ 4980

Fig. 3 (cont.)

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GGTGTTCATATGAAATGTATTTTAAAACTTTAAAAACCACTCCGGAAAAGCAATAA  
 4981 -----+-----+-----+-----+-----+-----+ 5040  
 AAATCAAAACAACGTCACAATTCAAATTCAAAAGTTATTTCATCCGATTGTTTATTTTG  
 5041 -----+-----+-----+-----+-----+-----+ 5100  
 CAAAATTTGAAAAATCATGAAGGATTTAGAAAAGTTTATAACATTTTCTAGATTTT  
 5101 -----+-----+-----+-----+-----+-----+ 5160  
 TCAAAATTTTAAAAACAAATCGAGAAAAAGAGAATGAAAAATCGATTTTAAAAATATCC  
 5161 -----+-----+-----+-----+-----+-----+ 5220

Repeat 3

<=====

ACAGCTTCGAGAGTTTGAAATTACAGTACTCCTTAAAGGCGCACACCCCATTTGCATTGG  
 5221 -----+-----+-----+-----+-----+-----+ 5280

=====

ACCAAAAATTTGTCGTGTCGAGACCAGGTACCGTAGTTTTTGTGCGAAAAATTGCACCAT  
 5281 -----+-----+-----+-----+-----+-----+ 5340  
 TGGACAATAAACCTTCCTAATCACCAAAAAGTAAAATTGAAATCTTCGAAAAGCCAAAAA  
 5341 -----+-----+-----+-----+-----+-----+ 5400  
 ATTCAAAAAAAGTCGAATTTTCGATTTTTTTTTTGGTTTTTGGTCCCAAAAACCAAAA  
 5401 -----+-----+-----+-----+-----+-----+ 5460  
 AAATCAATTTTCTGCAAAATACCAAAAAGAAACCCGAAAAAATTTCCCAGCCTTGTTCTT  
 5461 -----+-----+-----+-----+-----+-----+ 5520

AATGTAAACTGATATTTAATTTCCAGGGAATGCTCCTGACAATTCGAGACTTTGCCAAAC  
 5521 -----+-----+-----+-----+-----+-----+ 5580

G M L L T I R D F A K H  
 290 300

ACGAATCACACGGAGATTCTGCGATACTCGTGATTCTATCACACGGAGAAGAGAATGTGA  
 5581 -----+-----+-----+-----+-----+-----+ 5640

E S H G D S A I L V I L S H G E E N V I  
 310 320

TTATTGGAGTTGATGATATACCGATTAGTACACACGAGATATATGATCTTCTCAACGCGG  
 5641 -----+-----+-----+-----+-----+-----+ 5700

I G V D D I P I S T H E I Y D L L N A A  
 330 340

A(n2433)  
 | | intron 5

CAAATGCTCCCCGTCTGGCGAATAAGCCGAAAATCGTTTTTGTGCAGGCTTGTCGAGGCG  
 5701 -----+-----+-----+-----+-----+-----+ 5760

N A P R L A N K P K I V F V Q A C R G E  
 350 360

GTTCGTTTTTTATTTTAAATTTTAATATAAATATTTTAAATAAATTCATTTTCAGAACGTC  
 5761 -----+-----+-----+-----+-----+-----+ 5820

R R

GTGACAATGGATTCCCAGTCTTGATTCTGTGACGGAGTTCCTGCATTCTTCGTCGTCG  
 5821 -----+-----+-----+-----+-----+-----+ 5880

D N G F P V L D S V D G V P A F L R R G  
 370 380

Fig. 3 (cont.)

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Repeat 5

=====  
CTTGAAACAAACAATGCATGTCTAACTTTTAAGGACACAGAAAAATAGGCAGAGGCTCCT  
6541 -----+-----+-----+-----+-----+-----+ 6600

=====>  
TTTGCAAGCCTGCCGCGCGTCAACCTAGAATTTTAGTTTTAGCTAAAAATGATTGATTTT  
6601 -----+-----+-----+-----+-----+-----+ 6660  
GAATATTTTATGCTAATTTTTCGTTAAATTTTGAAATAGTCACTATTTATCGGGTTT  
6661 -----+-----+-----+-----+-----+-----+ 6720  
CCAGTAAAAAATGTTTATTAGCCATTGGATTTTACTGAAAACGAAAATTTGTAGTTTTTC  
6721 -----+-----+-----+-----+-----+-----+ 6780  
AACGAAATTTATCGATTTTAAATGTAAAAAATAAGCGAAAATTACATCAACCATCAA  
6781 -----+-----+-----+-----+-----+-----+ 6840  
GCATTTAAGCCAAAATTGTTAACTCATTAAAAAATTAATTCAAAGTTGTCCACGAGTATT  
6841 -----+-----+-----+-----+-----+-----+ 6900

Repeat 5

<=====  
ACACGGTTGGCGCGCGGCAAGTTTGCAAACGACGCTCCGCCTCTTTTTCTGTGCGGCTT  
6901 -----+-----+-----+-----+-----+-----+ 6960

=====  
GAAAAACAAGGGATCGGTTTAGATTTTTCCCCAAAATTTAAATTAAATTTTCAGATGACATC  
6961 -----+-----+-----+-----+-----+-----+ 7020  
M T S

CCGCCTGCTCAAAAAGTTCTACTTTTGGCCGGAAGCACGAAACTCTGCCGTCTAAAATTC  
7021 -----+-----+-----+-----+-----+-----+ 7080  
R L L K K F Y F W P E A R N S A V \*  
490 500

ACTCGTGATTCATTGCCCAATTGATAATTGTCTGTATCTTCTCCCCAGTTCTCTTTCGC  
7081 -----+-----+-----+-----+-----+-----+ 7140  
CCAATTAGTTTAAACCATGTGTATATTGTTATCCTATACTCATTTCATTTTATCATTCT  
7141 -----+-----+-----+-----+-----+-----+ 7200  
ATCATTCTCTTCCATTTTACACATTTCCATTTCTCTACGATAATCTAAAATTATGAC  
7201 -----+-----+-----+-----+-----+-----+ 7260  
GTTTGTGTCTCGAACGCATAATAATTTTAATAACTCGTTTTGAATTTGATTAGTTGTTGT  
7261 -----+-----+-----+-----+-----+-----+ 7320  
GCCCAGTATATATGTATGTACTATGCTTCTATCAACAAAATAGTTTCATAGATCATCACC  
7321 -----+-----+-----+-----+-----+-----+ 7380  
CCAACCCACCAACCTACCGTACCATATTCATTTTTCGCGGAATCAATTTTCGATTAATT  
7381 -----+-----+-----+-----+-----+-----+ 7440  
TTAACCTATTTTTTCGCCACAAAAAATCTAATATTTGAATTAACGAATAGCATTCCCATC  
7441 -----+-----+-----+-----+-----+-----+ 7500  
TCTCCCGTGCCGGAATGCCTCCCGGCCTTTTAAAGTTTCGGAACATTTGGCAATTATGTAT  
7501 -----+-----+-----+-----+-----+-----+ 7560  
AAATTTGTAGGTCCCCCCCATCATTTCCCGCCCATCATCTCAAATTGCATTCTTTTTTTCG  
7561 -----+-----+-----+-----+-----+-----+ 7620  
CCGTGATATCCCGATTCTGGTCAGCAAAGATCT  
7621 -----+-----+-----+-----+-----+-----+ 7653

Fig. 3 (cont.)

0988490600  
T02290" C4288860

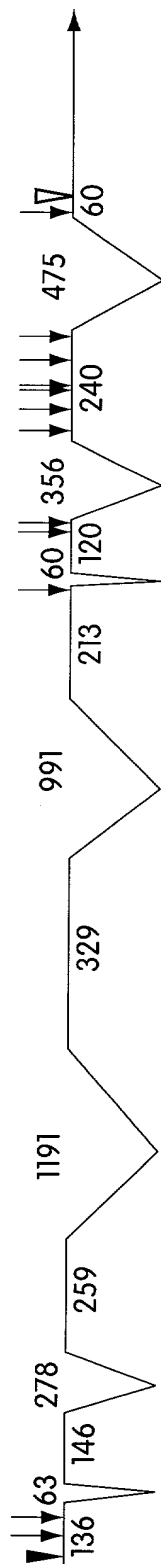


Fig. 4A

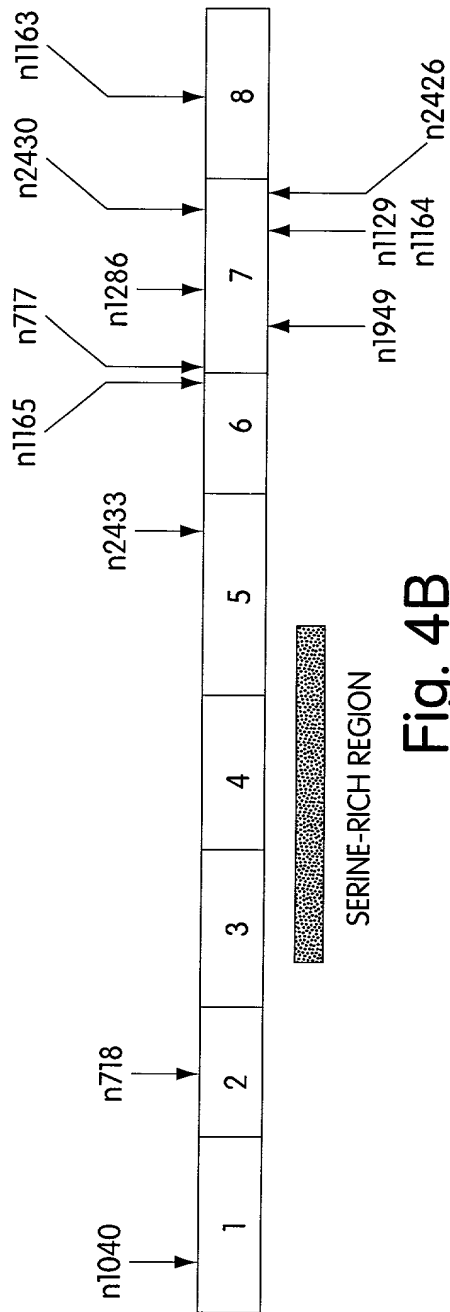


Fig. 4B

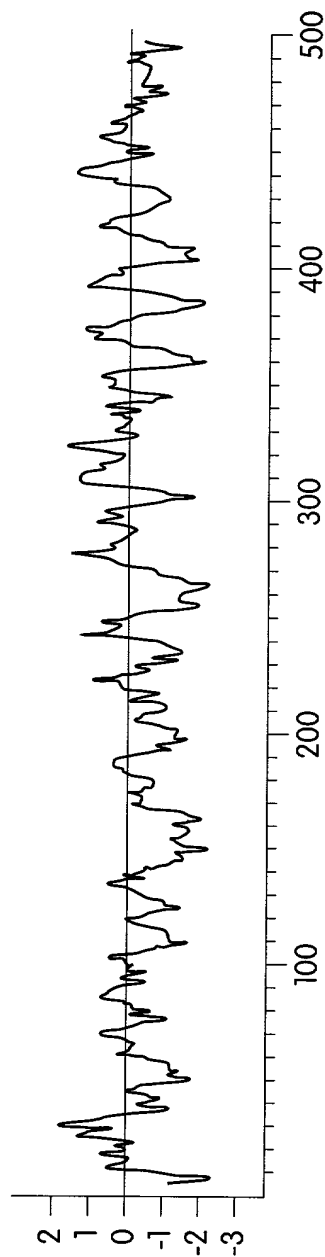


Fig. 5



ICE 167 IICNEEFDSIPRRTGAEVDITGMTMLLQNLGYSDVKKNLTASDMTTELE  
 || |||. : | |. |...| ..: | |. : |||. |. |. ||| : : | .. :  
 Ced-3 247 IINNEHF EQMPTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIR  
 BGAfQ =====

217 AFAHRPEHKTS DSTFLVFM SHGIREGICGKKHSEQVPDI.LQLNAIFNML  
 . |||. : | |. : ||| : ||| : ..|. |. ||| : .. : ||| :  
 297 DFAKHESH..GDSAILVILSHGEENVIIG.....VDDIPISTHEIYDLL

BGAfQ =====

active site autocleavage site  
 266 NTKNCPSLKD KPKV IIIQACRGDSPGVVW.FKDSVGVSGNLSLPTTEEFE  
 |. |. |. | : ||| : ||| : ||| : ||| : ..|. |. ||| : .. : ||| :  
 339 NAANAPRLANKPKIVFVQACRGERRDNGFPVLDSVDGVPAFLRRGWDNRD

↓  
S

BGAfQ =====

315 DDAI.....KKAHIEKDFIAFCSSSTPDNVSWRHPTMGSVFI  
 :. : : | . : | : : ..| : : ||| : ..| | |  
 389 GPLFNFLGCVRPQVQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFI  
 ↓ ↓  
 stop stop

351 GR LIEHMQEYACSCDVEEIF....RKVRFSFEQPDGRAQMPTT.ERVT.L  
 . :. | : ..| . || | : : : || : : : ..| .. :. | :. |  
 439 QAVCEVFSTHAKDMDVVELL TEVNKKVACGFQTSQGSNILKQMPMTSRL  
 ↓ ↓ ↓ ↓  
 V V K F

395 TRCFYLFPGH\*.... 404  
 : || : : :  
 489 LKKFYFWPEARNSAV 503

Fig. 6A (cont.)

# Alignment of Ced-3 and Murine NEDD-2

Ced-3	251	EHFEQMPTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIRDFAK	300
NEDD-2	1	.....: : : :	9
		.....MLTVQVVRT	
	301	HESHGDSAILVILSHGEENVIIIGVDDIPISTHEIYDILLNAANAPRLANKP	350
	10	..: : : : : : : : :	37
		SQKCSSSKHV.....EVLLD....PLGT.SFCSLL.....PP	
	351	KIVFVQACRGERRDNGFPVLDSVDGVPFLRRGWDNRDGPLFNLGCVRP	400
	38	...: : : : : : : : :	73
		PLLLYETDRGVDQDGKNHTQSPGC.....EESDAGKEELM.....	
	401	QVQQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFIQAVCEVFSTHAK	450
	74	...: : : : : : : : :	118
		.....KMRLPTRSDMICGYACLKGNAMRNRTKRGSWYIEALTQVFSEAC	
		n2426 K F n1163	
	451	DMDVVELLTEVNK..KVACGFQTSQGSNLLKQMPMTSRLLKKFYFWPEA	498
	119	: : : : : : : : : : :	168
		DMHVADMLVKVNALIKEREGYAPGTEFHRCKEMSEYCSLCCQLYLFPGY	
	499	RNSAV	503
	169	PPT...	172

Fig. 6B

## Alignment of N-terminal regions of ced-3/ICE- related proteins

c. briggsae ced-3	MMRQDRWSLLERNILEFSKQLQADLILDVLI	AKQVLNSDNGDVINSCTERDNEKEIVKAVQRRGDEAFADYDALRDTGHNDLADVLMPLSR	----PNPV
ced-3 protein	MMRQDRSLLERNIMFSSHLKVDEILEVLI	AKQVLNSDNGDMINSCTVREKRREIVKAVQRPDVAFDAFYDALRSTGEGHAEVLEPLARSVDNAV	100
C. vulgaris ced-3	-----	-----	-----
Mouse ICE.gw	M-----ADKIL-----	RAKRKQFINSV-----SIGTINGLLDELLEK-----	RVLNQEEM-----DKI
Human ICE.GW	M-----ADKVL-----	KEKRKLFRSM-----GEGTINGLLDELLQT-----	RVLNKEEM-----EKV
Consensus	M.....AD..IL.....	.....R.KRK.....V...G.....D.L..T.....VL.....	....V
c. briggsae ced-3	PMECPMSPSHRRSRALSPPGYASPTRVHRDSISSVSFTSTYQDVYSRRSSSRPLQSSDRHNVSAA	-TSFPSPQSSANSSTFTGCASLGYSSSRN	198
ced-3 protein	EFECMPSPASHRRSRALSPAGYTSPTRVHRDSVSVSFTSYQD	-IYSRARSRSR-RALHSSDRHNYSPPVNAFPSPQSSANSSTFTGCSSSLGYSSSRN	198
C. vulgaris ced-3	-----	-----	-----
Mouse ICE.gw	KLA---NITAMDKARDLCDHVSKKGPQASQIFITYICNEDCYL	-----AGILELQSAPE--TFVAT-----	EDSKGHPSSSETKEEQNKED-G
Human ICE.GW	KRE---NATVMDKTRALIDSVIPKGAQCQICITYICEEDSYL	-----AGTLGLSADQTSQ--NYLNM-----	QDSQGLSSFPAPQAVQDNPAMP
Consensus	..E-----RAL.....I.....SY..	-----S.SRS.R.L.SSDRHN.Y.S...F.SQP.SANSSTFTG.-SLGYSSSR.	
c. briggsae ced-3	RSFSKTSAQSQYIFHEEDMNYVDAPTHRVFDEKTYRNFSPPRGCLII	INNEHTEQMPTRNGTKAKDNLTNIFRCMGYTVICKNLTGRENLTIRSF	298
ced-3 protein	RSFSKASGPTQYIFHEEDMNFVDAPISRVFDEKTYRNFSPPRGCLII	INNEHTEQMPTRNGTKAKDNLTNIFRCMGYTVICKNLTGRCMLLTIRDF	298
C. vulgaris ced-3	RSYSKASAHSQYIFHEEDMNYVDAPTHRVFDEKTYRNFSPPRGCLII	INNEHTEQMPTRNGTKPKDNISNLFRCMGYIVHCKDNLTGRMML-TIRDF	
Mouse ICE.gw	TFPGLTGTLKFCPLEKAQKLWKENPS--EII--PIANTT-TRTR-LALII	ICNTFFQHLSPRVGAQVDLEMKLLLEDLGYTWKVKENLTALEMVKEVKEF	
Human ICE.GW	TSSGSEGNVKLCSLEAQRIWKQKSA--EII--PIMDKS-SRTR-LALII	ICNEETDSIPRRTGAEVDITGWTMLLQNLGYSVDVKKNLTASDMTTELEAF	
Consensus	RS.SK.S...QYIFHEEDMN.VDAPTI.RVFDEKTYRNFSPPRGCLII	INNEHTEQMPTRNGTK.DKDN.TNIFRCMGYTV.CKDNLTGR.ML.TIR..F	
c. briggsae ced-3	GRNDME--GDSAILVTLSHGEENVIIIG	---VDDVS--VNVHETVDLINAANAPRLANKPKLVFVQACRG	
ced-3 protein	AKHESH--GDSAILVTLSHGEENVIIIG	---VDDIP--ISTHETVDLINAANAPRLANKPKLVFVQACRG	
C. vulgaris ced-3	AKNETH--GDSAILVTLSHGEENVIIIG	---VDDVS--VNVHETVDLINAANAPRLANKPKLVFVQACRG	
Mouse ICE.gw	AACPETHKTSDFLVMFMSHGIQEGICGTYTSNEVSDILKVDITFQMMNTLNCPSLKD	KPKVIIIQACRG	
Human ICE.GW	AARPEHKTSDSTFLVMFMSHGIQEGICGKKHSEQVPDILQLNALIFNMINTKNCPSLKD	KPKVIIIQACRG	
Consensus	A....H...CDSAILVTLSHGEENVIIIG	---VDDVS--..VHEIVDILINAANAPRLANKPKLVFVQACRG	

Fig. 6C

# Alignment of C-terminal regions of ced-3/ICE/NEDD-2 - related proteins

ICE C-terminus	DSPGVW---	-----	--FKDSVG--	-----	-----V
Mouse ICE C-ter	EKQGWL---	-----	--LKDSVR--	-----	-----D
C.briggsae C-ter	ERRDNGFP--	-----	--VLDSDVG--	-----VPSLI	-----RRGWDN
ced-3 C-terminus	ERRDNGFP--	-----	--VLDSDVG--	-----VPAFL	-----RRGWDN 386
C. vulgaris C-terminus	ERRDVGFP--	-----	--VLDSDVG--	-----VPALI	-----RRGWDK
nedd-2 protein.gw	MLTVQVYRTS	QKCSSSKHV	EVLLDPLGTS	FCSLLPPPLL	LYETDRGVDDQ
Consensus	E.....	-----	--LDSV..	-----P...	-----RG.D.
ICE C-terminus	SGNL---SLP	TTEEFE---	DAIKKA-HIE	KDFIAFCSST	PDNVSWRHPT
Mouse ICE C-ter	SEE-----DFL	TDAIFE---	DGIKKA-HIE	KDFIAFCSST	PDNVSWRHPT
C.briggsae C-ter	RDG-PLFNFL	GCVRPQV--Q	QVWRKK-PSQ	ADMLIAYATT	AQYVSWRNSA
ced-3 C-terminus	RDG-PLFNFL	GCVRPQV--Q	QVWRKK-PSQ	ADILLIAYATT	AQYVSWRNSA 432
C. vulgaris C-terminus	GDG-P--NFL	GCVRPQA--Q	QVWRKK-PSQ	ADILLIAYATT	AQYVSWRNSA
nedd-2 protein.gw	QDGKNHTQSP	GCEESDAGKE	ELMKRLPTR	SDMICGYACL	KGNAAMRNTK
Consensus	.DG---.FL	GC.....	....K.-P..	.D....YA.T	...VSWRN..
ICE C-terminus	MGSVFIQRLI	EHMQEYACSC	DVEEIFRKV-	-RF----	SFE QPDGRAQMPT
Mouse ICE C-ter	RGSLFIESLI	KHMKEYAWSC	DLEDIFRKV-	-RF----	SFE QPEFRLQMPT
C.briggsae C-ter	RGSWFIQAVC	EVFSLHAKDM	DVVELLTEVN	KKVA--CGFQ	TSQGSNILKQ
ced-3 C-terminus	RGSWFIQAVC	EVFSTHAKDM	DVVELLTEVN	KKVA--CGFQ	TSQGSNILKQ 480
C. vulgaris C-terminus	RGSWFIQAVC	EVFSLHAKDM	DVVELLTEVN	KKVA--CGFQ	TSQGANILKQ
nedd-2 protein.gw	RGSWYIEALT	QVFSEACDM	HVADMLVXVN	ALIKEREGYA	PGTEFHRCKE
Consensus	RGS.FI.A..	EVFS..A.DM	DV.E.L..V.	.....GF.	...G....K.
ICE C-terminus	T-ERVTLTR	CFYLPFGH--	-----	-----	-----
Mouse ICE C-ter	A-DRVT-LTK	RFYLPFGH--	-----	-----	-----
C.briggsae C-ter	MPELTSRLK	KFYFWPEDRG	RNSAV	-----	-----
ced-3 C-terminus	MPELTSRLK	KFYFWPEAR-	-NSAV	503	
C. vulgaris C-terminus	MPELTSRLK	KFYFWPEDRN	RSSAV	-----	-----
nedd-2 protein.gw	MSEYCSLTCQ	QLYLPFG---	-YPPT	-----	-----
Consensus	M.E..S..L.K	.FY..P..	-----	-----	-----

Fig. 6D



Lines

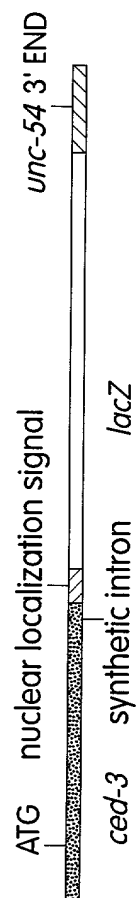
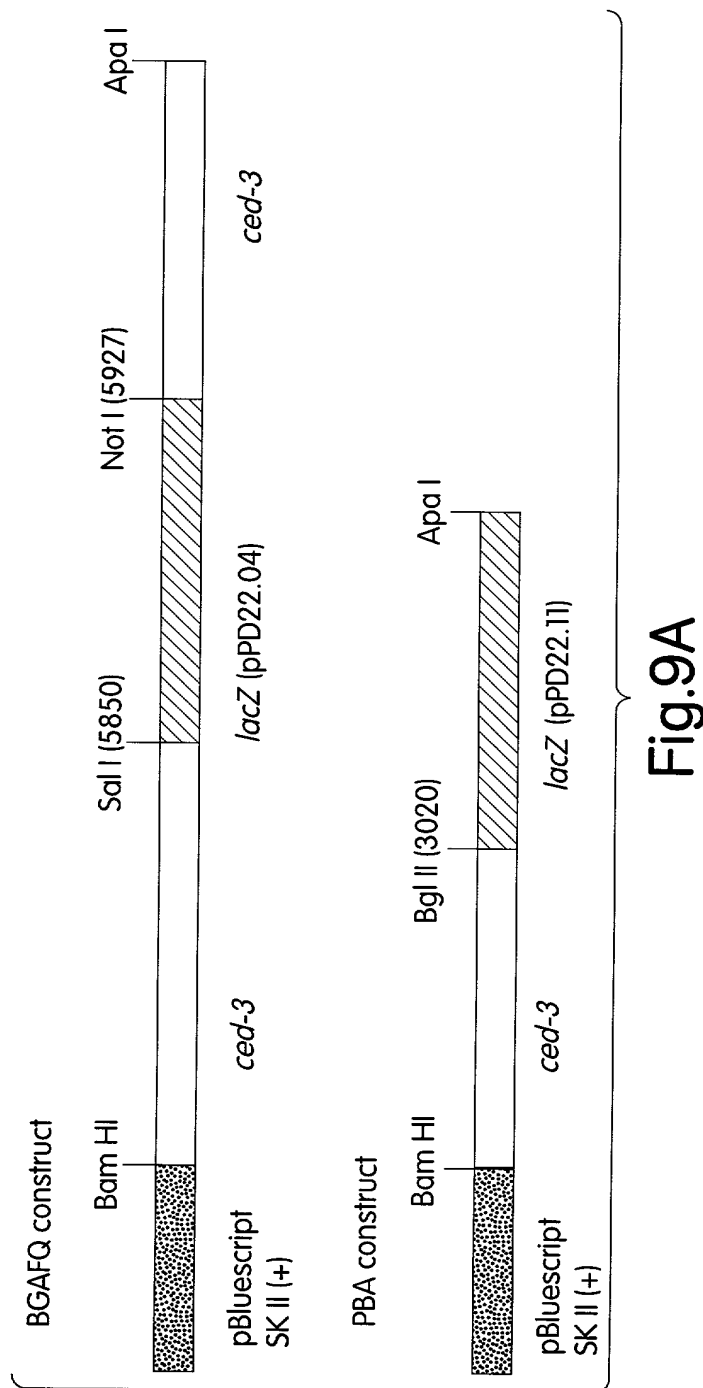
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 2 .....W\_.....LE...K.QA.L..D.....V....R.E  
 3 TVSISLI..R..... M.....  
  
 1 51 REKRREIVKAVQRPQDVAFDADFALRSTGHEGLAEVLEPLARSVDSNAV 100  
 2 .DNEK.....R..E.....D...ND..D..M..S.P .P.  
 3  
  
 1 101 EFECPMSPASHRRSRALSPAGYTSPTVRHDSVSSVSSFTS\_YQDIYSRA 149  
 2 PM.....S.....P .A.....I.....T...V....  
 3 S  
  
 1 150 RSRSR\_SRALHSSDRHNYSSPPVNAFSPQSSANSSTGCSSLGYSSSRN 198  
 2 ..S..S..P.Q.....M.AA\_TS.....A.....  
 3 T...\_\_..P..T.....V..S..S.Q...A.....S.....T  
  
 1 199 RSFSKASGPTQYIFHEEDMNFVDAPTISR VFDEKTMYNFSSPRGMCLI 247  
 2 .....T.AQS.....Y.....H.....L...  
 3 ..Y....AHS.....Y.....H.....T...L...  
  
 1 248 INNEHFQMPTRNGTKADKDNLTNLFRCMGYTVICKDNLTGRGMLLTIRD 297  
 2 .....I.....E..S...S  
 3 .....P....IS.....I.H.....M.....  
  
 1 298 FAKHESHGDSAILVILSHGEENVIGVDDIPISTHEIYDLLNAANAPRLA 347  
 2 .GRNDM.....VSVNV.....  
 3 ...N.T.....VSVNV....x.....  
  
 1 348 NKPKIVFVQACRGERRDNGFPVLDSVDGVPAFLRRGWDNRDGPLFNFLGC 397  
 2 ....L.....SLI.....  
 3 ....L.....V.....LI....KG...  
  
 1 398 VRPQVQQVWRKKPSQADILIRYATTAQYVSWRNSARGSWFIQAVCEVFST 447  
 2 .....M..A.....L  
 3 ....A.....A.....L  
  
 1 448 HAKDMDVVELLTEVNKKVACGFQTSQGSNILKQMPEMTSRLLKKFYFWPE 497  
 2 .....L.....  
 3 .....A.....L.....  
  
 1 498 \_\_ARN\_\_SAV 503  
 2 DRG...  
 3 \_\_D..RS...

Fig. 7

Interleukin-1 $\beta$  convertase cDNA sequence

1 AAAAGGAGAG AAAAGCCATG GCCGACAAGG TCCTGAAGGA GAAGAGAAAG  
 51 CTGTTTATCC GTTCCATGGG TGAAGGTACA ATAAATGGCT TACTGGATGA  
 101 ATTATTACAG ACAAGGGTGC TGAACAAGGA AGAGATGGAG AAAGTAAAC  
 151 GTGAAAATGC TACAGTTATG GATAAGACCC GAGCTTTGAT TGACTCCGTT  
 201 ATTCCGAAAG GGGCACAGGC ATGCCAAATT TGCATCACAT ACATTTGTGA  
 251 AGAAGACAGT TACCTGGCAG GGACGCTGGG ACTCTCAGCA GATCAAACAT  
 301 CTGGAAATTA CCTTAATATG CAAGACTCTC AAGGAGTACT TTCTTCCTTT  
 351 CCAGCTCCTC AGGCAGTGCA GGACAACCCA GCTATGCCCA CATCCTCAGG  
 401 CTCAGAAGGG AATGTCAAGC TTTGCTCCCT AGAAGAAGCT CAAAGGATAT  
 451 GGAAACAAAA GTCGGCAGAG ATTTATCCAA TAATGGACAA GTCAAGCCGC  
 501 ACACGTCTTG CTCTCATTAT CTGCAATGAA GAATTTGACA GTATTCCTAG  
 551 AAGAACTGGA GCTGAGGTTG ACATCACAGG CATGACAATG CTGCTACAAA  
 601 ATCTGGGGTA CAGCGTAGAT GTGAAAAAAA ATCTCACTGC TTCGGACATG  
 651 ACTACAGAGC TGGAGGCATT TGCACACCGC CCAGAGCACA AGACCTCTGA  
 701 CAGCACGTTT CTGGTGTTCA TGTCTCATGG TATTCGGGAA GGCATTTGTG  
 751 GGAAGAAACA CTCTGAGCAA GTCCCAGATA TACTACAACT CAATGCAATC  
 801 TTAAACATGT TGAATACCAA GAACTGCCCA AGTTTGAAGG ACAAACCGAA  
 851 GGTGATCATC ATCCAGGCCT GCCGTGGTGA CAGCCCTGGT GTGGTGTGGT  
 901 TTAAAGATTG AGTAGGAGTT TCTGGAAACC TATCTTTACC AACTACAGAA  
 951 GAGTTTGAGG ATGATGCTAT TAAGAAAGCC CACATAGAGA AGGATTTTAT  
 1001 CGCTTTCTGC TCTTCCACAC CAGATAATGT TTCTTGGAGA CATCCCACAA  
 1051 TGGGCTCTGT TTTTATTGGA AGACTCATTG AACATATGCA AGAATATGCC  
 1101 TGTTCCCTGTG ATGTGGAGGA AATTTTCCGC AAGGTTGAT TTTCAATTTGA  
 1151 GCAGCCAGAT GGTAGAGCGC AGATGCCAC CACTGAAAGA GTGACTTTGA  
 1201 CAAGATGTTT CTACCTCTTC CCAGGACATT AAAATAAGGA AACTGTATGA  
 1251 ATGTCTGCGG GCAGGAAGTG AAGAGATCGT TCTGTAAAAG GTTTTTGGAA  
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 1351 AAATGAAAAA AAAAAAAAAA AAA

Fig. 8



**Fig. 9B**

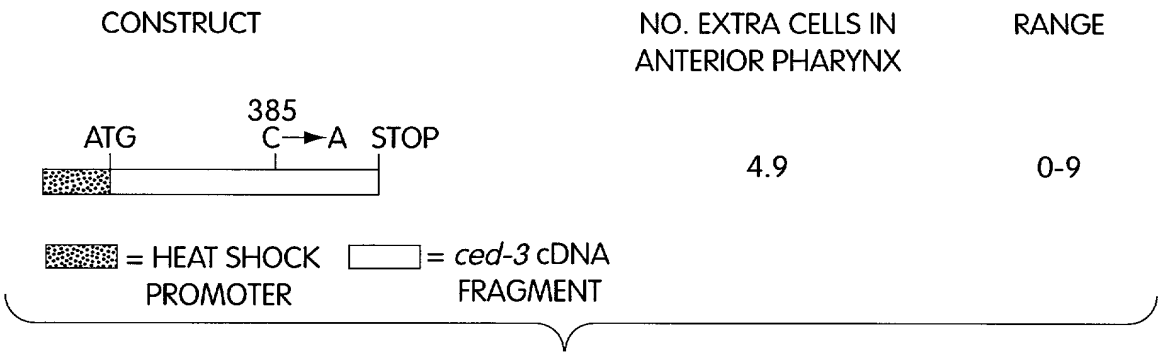


Fig. 10

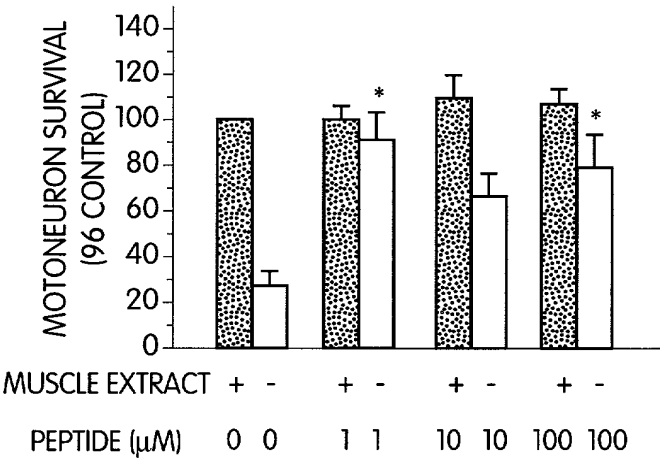


Fig. 11A

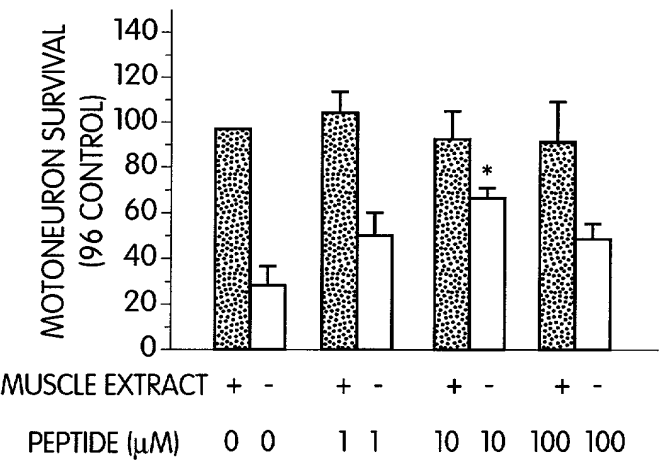


Fig. 11B

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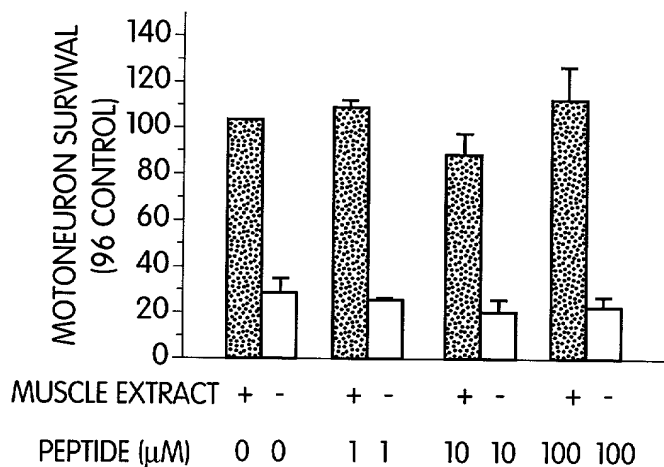


Fig. 11C

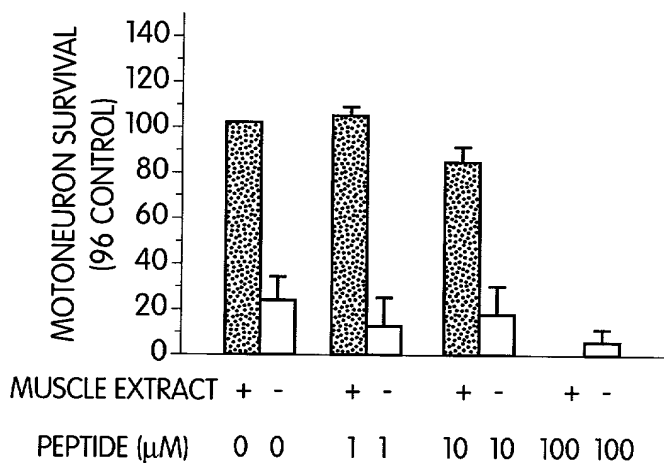


Fig. 11D

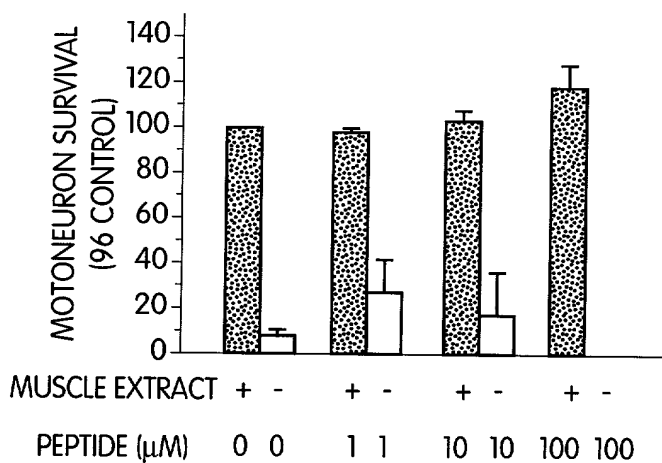
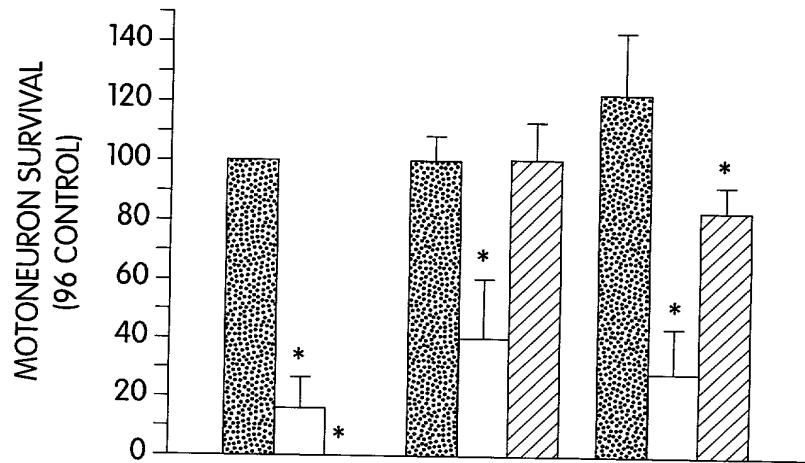
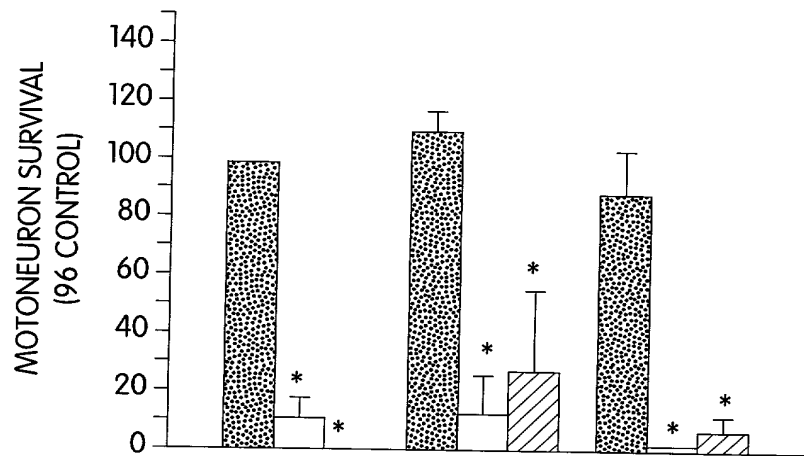


Fig. 11E



MUSCLE EXTRACT AT PLATING	+	-	-	+	-	-	+	-	-
PEPTIDE (μM)	0	0	0	1	1	1	10	10	10
MUSCLE EXTRACT AT 72 Hrs.	-	-	+	-	-	+	-	-	+

Fig. 12A



MUSCLE EXTRACT AT PLATING	+	-	-	+	-	-	+	-	-
PEPTIDE (μM)	0	0	0	1	1	1	10	10	10
MUSCLE EXTRACT AT 72 Hrs.	-	-	+	-	-	+	-	-	+

Fig. 12B

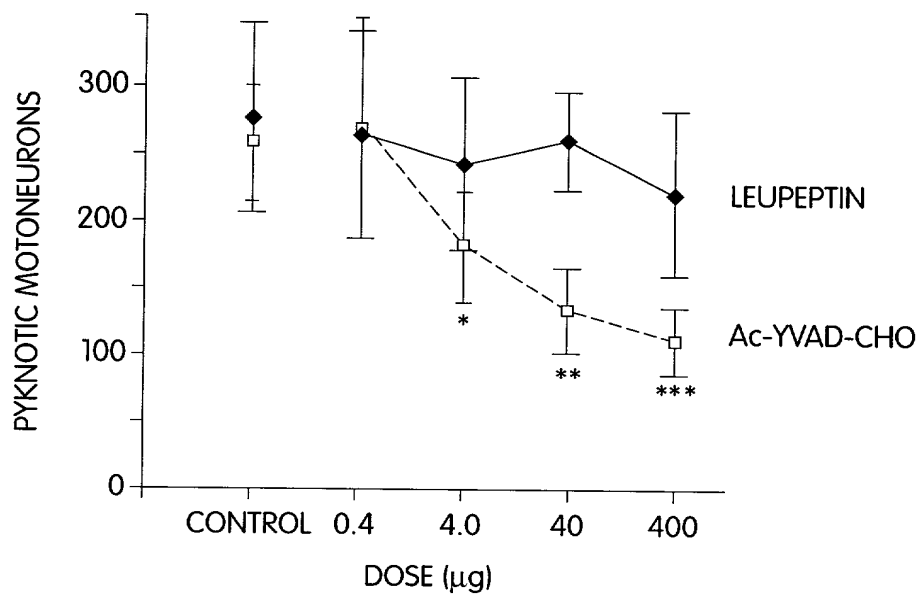


Fig. 13

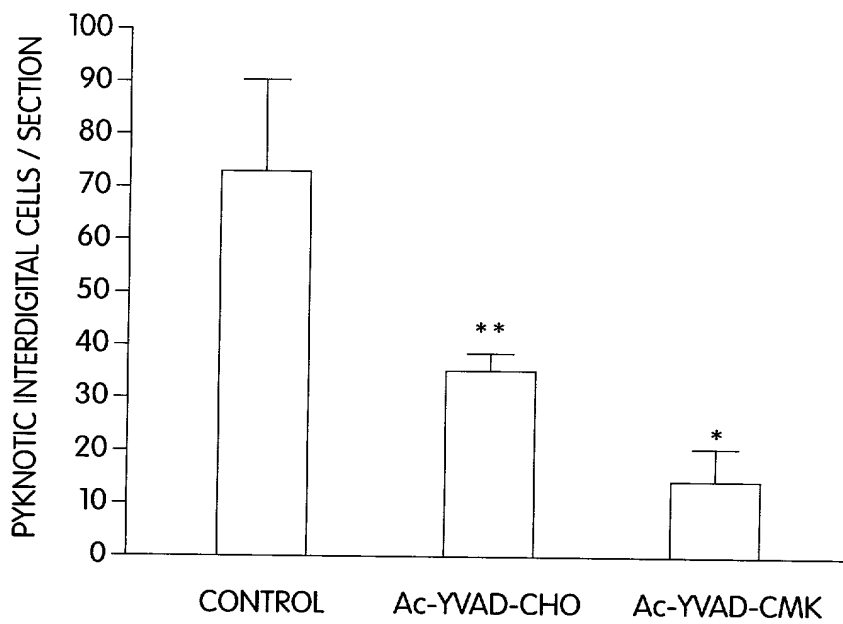


Fig. 14

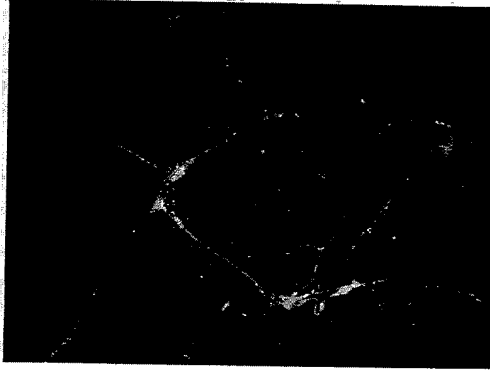


Fig. 15C



Fig. 15D

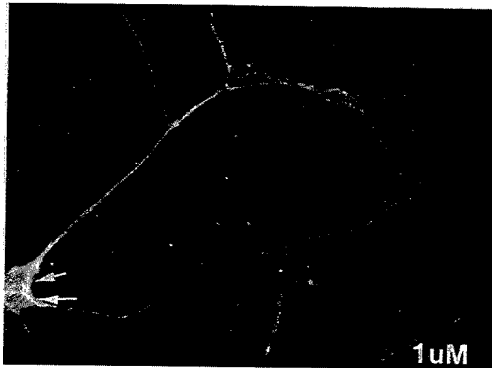


Fig. 15E

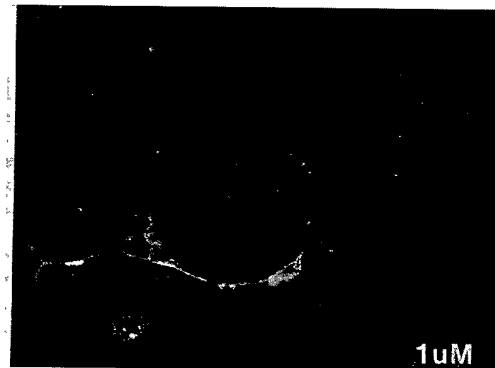


Fig. 15F

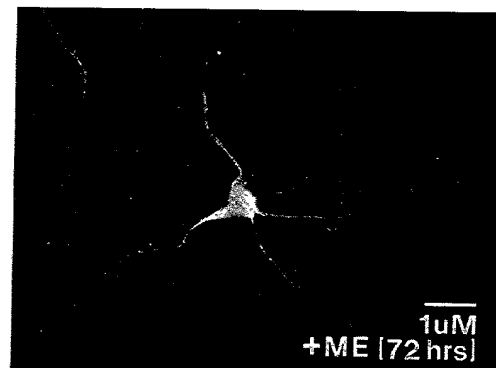


Fig. 15G